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SEP 0 3 2002

TECH CENTER 1600/2900

1600

RAW SEQUENCE LISTING   DATE: 08/22/2002
PATENT APPLICATION: US/09/810,836B   TIME: 16:45:23

Input Set : A:\SEQLIST514442001200.TXT
Output Set: N:\CRF3\08222002\I810836B.raw

ENTERED

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 4 <110> APPLICANT: Broun, Pierre
 6 <120> TITLE OF INVENTION: METHOD FOR MODIFYING A BIOSYNTHETIC
 7        PATHWAY
 9 <130> FILE REFERENCE: 514442001200/MBI0032
11 <140> CURRENT APPLICATION NUMBER: US 09/810,836B
12 <141> CURRENT FILING DATE: 2001-03-16
14 <160> NUMBER OF SEQ ID NOS: 18
16 <170> SOFTWARE: FastSEQ for Windows Version 4.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1239
20 <212> TYPE: DNA
21 <213> ORGANISM: Arabidopsis thaliana
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (6)...(1091)
26 <223> OTHER INFORMATION: G993
28 <400> SEQUENCE: 1
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30       Met Glu Tyr Ser Cys Val Asp Asp Ser Ser Thr Thr Ser Glu Ser
31        1           5                   10                  15
33 ctc tcc atc tct act act cca aag ccg aca acg acg acg gag aag aaa      98
34 Leu Ser Ile Ser Thr Thr Pro Lys Pro Thr Thr Thr Thr Glu Lys Lys
35              20                  25                  30
37 ctc tct tct ccg ccg gcg acg tcg atg cgt ctc tac aga atg gga agc     146
38 Leu Ser Ser Pro Pro Ala Thr Ser Met Arg Leu Tyr Arg Met Gly Ser
39          35                  40                  45
41 ggc gga agc agc gtc gtt ttg gat tca gag aac ggc gtc gag acc gag     194
42 Gly Gly Ser Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Thr Glu
43          50                  55                  60
45 tca cgt aag ctt cct tcg tcg aaa tat aaa ggc gtt gtg cct cag cct     242
46 Ser Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro
47       65                  70                  75
49 aac gga aga tgg gga gct cag att tac gag aag cat cag cga gtt tgg     290
50 Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp
51 80                  85                  90                  95
53 ctc ggt act ttc aac gag gaa gaa gaa gct gcg tct tct tac gac atc     338
54 Leu Gly Thr Phe Asn Glu Glu Glu Glu Ala Ala Ser Ser Tyr Asp Ile
55              100                 105                 110
57 gcc gtg agg aga ttc cgc ggc cgc gac gcc gtc act aac ttc aaa tct     386
58 Ala Val Arg Arg Phe Arg Gly Arg Asp Ala Val Thr Asn Phe Lys Ser
59              115                 120                 125
61 caa gtt gat gga aac gac gcc gaa tcg gct ttt ctt gac gct cat tct     434
62 Gln Val Asp Gly Asn Asp Ala Glu Ser Ala Phe Leu Asp Ala His Ser
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63          130                  135                  140
65 aaa gct gag atc gtg gat atg ttg agg aaa cac act tac gcc gat gag        482
66 Lys Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Ala Asp Glu
67     145                  150                  155
69 ttt gag cag agt aga cgg aag ttt gtt aac ggc gac gga aaa cgc tct        530
70 Phe Glu Gln Ser Arg Arg Lys Phe Val Asn Gly Asp Gly Lys Arg Ser
71 160                  165                  170                  175
73 ggg ttg gag acg gcg acg tac gga aac gac gct gtt ttg aga gcg cgt        578
74 Gly Leu Glu Thr Ala Thr Tyr Gly Asn Asp Ala Val Leu Arg Ala Arg
75                  180                  185                  190
77 gag gtt ttg ttc gag aag act gtt acg ccg agc gac gtc ggg aag ctg        626
78 Glu Val Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu
79              195                  200                  205
81 aac cgt tta gtg ata ccg aaa caa cac gcg gag aag cat ttt ccg tta        674
82 Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu
83         210                  215                  220
85 ccg gcg atg acg acg gcg atg ggg atg aat ccg tct ccg acg aaa ggc        722
86 Pro Ala Met Thr Thr Ala Met Gly Met Asn Pro Ser Pro Thr Lys Gly
87     225                  230                  235
89 gtt ttg att aac ttg gaa gat aga aca ggg aaa gtg tgg cgg ttc cgt        770
90 Val Leu Ile Asn Leu Glu Asp Arg Thr Gly Lys Val Trp Arg Phe Arg
91 240                  245                  250                  255
93 tac agt tac tgg aac agc agt caa agt tac gtg ttg acc aag ggc tgg        818
94 Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp
95                  260                  265                  270
97 agc cgg ttc gtt aaa gag aag aat ctt cga gcc ggt gat gtg gtt tgt        866
98 Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val Cys
99              275                  280                  285
101 ttc gag aga tca acc gga cca gac cgg caa ttg tat atc cac tgg aaa       914
102 Phe Glu Arg Ser Thr Gly Pro Asp Arg Gln Leu Tyr Ile His Trp Lys
103         290                  295                  300
105 gtc cgg tct agt ccg gtt cag act gtg gtt agg cta ttc gga gtc aac      962
106 Val Arg Ser Ser Pro Val Gln Thr Val Val Arg Leu Phe Gly Val Asn
107     305                  310                  315
109 att ttc aat gtg agt aac gag aaa cca aac gac gtc gca gta gag tgt      1010
110 Ile Phe Asn Val Ser Asn Glu Lys Pro Asn Asp Val Ala Val Glu Cys
111 320                  325                  330                  335
113 gtt ggc aag aag aga tct cgg gaa gat gat ttg ttt tcg tta ggg tgt      1058
114 Val Gly Lys Lys Arg Ser Arg Glu Asp Asp Leu Phe Ser Leu Gly Cys
115              340                  345                  350
117 tcc aag aag cag gcg att atc aac atc ttg tga caaattcttt ttttttggtt   1111
118 Ser Lys Lys Gln Ala Ile Ile Asn Ile Leu  *
119              355                  360
121 tttttcttca atttgtttct ccttttcaa tattttgtat tgaaatgaca agttgtaaat    1171
122 taggacaaga caagaaaaaa tgacaactag acaaatagt ttttgtttaa aaaaaaaaa     1231
123 aaaaaaaa                                                           1239
125 <210> SEQ ID NO: 2
126 <211> LENGTH: 361
127 <212> TYPE: PRT
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Input Set : A:\SEQLIST514442001200.TXT
Output Set: N:\CRF3\08222002\I810836B.raw

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130 <400> SEQUENCE: 2
131 Met Glu Tyr Ser Cys Val Asp Asp Ser Ser Thr Thr Ser Glu Ser Leu
132 1               5                   10                  15
133 Ser Ile Ser Thr Thr Pro Lys Pro Thr Thr Thr Thr Glu Lys Lys Leu
134             20                  25                  30
135 Ser Ser Pro Pro Ala Thr Ser Met Arg Leu Tyr Arg Met Gly Ser Gly
136         35                  40                  45
137 Gly Ser Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Thr Glu Ser
138     50                  55                  60
139 Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro Asn
140 65                  70                  75                  80
141 Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp Leu
142             85                  90                  95
143 Gly Thr Phe Asn Glu Glu Glu Glu Ala Ala Ser Ser Tyr Asp Ile Ala
144             100                 105                 110
145 Val Arg Arg Phe Arg Gly Arg Asp Ala Val Thr Asn Phe Lys Ser Gln
146         115                 120                 125
147 Val Asp Gly Asn Asp Ala Glu Ser Ala Phe Leu Asp Ala His Ser Lys
148     130                 135                 140
149 Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Ala Asp Glu Phe
150 145                 150                 155                 160
151 Glu Gln Ser Arg Arg Lys Phe Val Asn Gly Asp Gly Lys Arg Ser Gly
152             165                 170                 175
153 Leu Glu Thr Ala Thr Tyr Gly Asn Asp Ala Val Leu Arg Ala Arg Glu
154             180                 185                 190
155 Val Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu Asn
156         195                 200                 205
157 Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu Pro
158     210                 215                 220
159 Ala Met Thr Thr Ala Met Gly Met Asn Pro Ser Pro Thr Lys Gly Val
160 225                 230                 235                 240
161 Leu Ile Asn Leu Glu Asp Arg Thr Gly Lys Val Trp Arg Phe Arg Tyr
162             245                 250                 255
163 Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser
164             260                 265                 270
165 Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val Cys Phe
166         275                 280                 285
167 Glu Arg Ser Thr Gly Pro Asp Arg Gln Leu Tyr Ile His Trp Lys Val
168     290                 295                 300
169 Arg Ser Ser Pro Val Gln Thr Val Val Arg Leu Phe Gly Val Asn Ile
170 305                 310                 315                 320
171 Phe Asn Val Ser Asn Glu Lys Pro Asn Asp Val Ala Val Glu Cys Val
172             325                 330                 335
173 Gly Lys Lys Arg Ser Arg Glu Asp Asp Leu Phe Ser Leu Gly Cys Ser
174         340                 345                 350
175 Lys Lys Gln Ala Ile Ile Asn Ile Leu
176         355                 360
178 <210> SEQ ID NO: 3
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RAW SEQUENCE LISTING   DATE: 08/22/2002
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Input Set : A:\SEQLIST514442001200.TXT
Output Set: N:\CRF3\08222002\I810836B.raw

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179 <211> LENGTH: 1226
180 <212> TYPE: DNA
181 <213> ORGANISM: Arabidopsis thaliana
183 <220> FEATURE:
184 <221> NAME/KEY: CDS
185 <222> LOCATION: (111)...(989)
186 <223> OTHER INFORMATION: G1845
188 <400> SEQUENCE: 3
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190 ttttggcaaa tcgtgaactg ccacgtcttt aaggcatcag tgaagcaaag atg gac      116
191                                                        Met Asp
192                                                          1
194 ttt gac gag gag cta aat ctt tgt att acg aaa ggt aaa aat gtt gat    164
195 Phe Asp Glu Glu Leu Asn Leu Cys Ile Thr Lys Gly Lys Asn Val Asp
196          5                  10                  15
198 cat tct ttt gga gga gaa gct tct tcc acg tcc cca aga tct atg aag    212
199 His Ser Phe Gly Gly Glu Ala Ser Ser Thr Ser Pro Arg Ser Met Lys
200         20                  25                  30
202 aaa atg aag agt cct agt cgt cct aaa ccc tat ttc caa tcc tct tct    260
203 Lys Met Lys Ser Pro Ser Arg Pro Lys Pro Tyr Phe Gln Ser Ser Ser
204  35                  40                  45                  50
206 tct cct tat tcg tta gag gct ttc cct ttt tct ctc gat cca aca ctt    308
207 Ser Pro Tyr Ser Leu Glu Ala Phe Pro Phe Ser Leu Asp Pro Thr Leu
208                 55                  60                  65
210 cag aat cag caa caa caa ctc gga tca tac gtt ccg gta ctt gag caa    356
211 Gln Asn Gln Gln Gln Gln Leu Gly Ser Tyr Val Pro Val Leu Glu Gln
212             70                  75                  80
214 cga caa gac ccg aca atg caa ggc cag aag caa atg atc tcc ttt agt    404
215 Arg Gln Asp Pro Thr Met Gln Gly Gln Lys Gln Met Ile Ser Phe Ser
216             85                  90                  95
218 cct caa caa caa caa cag cag cag cag tat atg gcc cag tac tgg agt    452
219 Pro Gln Gln Gln Gln Gln Gln Gln Gln Tyr Met Ala Gln Tyr Trp Ser
220     100                 105                 110
222 gac aca ttg aat ctg agt cca aga gga aga atg atg atg atg atg agc    500
223 Asp Thr Leu Asn Leu Ser Pro Arg Gly Arg Met Met Met Met Met Ser
224 115                 120                 125                 130
226 caa gaa gct gtt caa cct tac atc gca acg aag ctg tac aga gga gtg    548
227 Gln Glu Ala Val Gln Pro Tyr Ile Ala Thr Lys Leu Tyr Arg Gly Val
228                 135                 140                 145
230 aga caa cgt caa tgg gga aaa tgg gtc gca gag atc cgt aag cca cga    596
231 Arg Gln Arg Gln Trp Gly Lys Trp Val Ala Glu Ile Arg Lys Pro Arg
232             150                 155                 160
234 agc agg gca cgt ctt tgg ctt ggt acc ttt gat aca gct gaa gaa gct    644
235 Ser Arg Ala Arg Leu Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala
236         165                 170                 175
238 gcc atg gcc tac gac cgc caa gcc ttc aaa tta cga ggc cac agc gca    692
239 Ala Met Ala Tyr Asp Arg Gln Ala Phe Lys Leu Arg Gly His Ser Ala
240     180                 185                 190
242 aca ctg aat ttc ccg gag cat ttt gtg aat aag gaa agc gag ctg cat    740
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Input Set : A:\SEQLIST514442001200.TXT
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243 Thr Leu Asn Phe Pro Glu His Phe Val Asn Lys Glu Ser Glu Leu His
244 195               200               205               210
246 gat tca aac tcg tcg gat cag aaa gaa cct gaa acg cca cag cca agc          788
247 Asp Ser Asn Ser Ser Asp Gln Lys Glu Pro Glu Thr Pro Gln Pro Ser
248               215               220               225
250 gag gtt aac ttg gag agc aag gaa cta ccg gtg att gat gtt ggg aga          836
251 Glu Val Asn Leu Glu Ser Lys Glu Leu Pro Val Ile Asp Val Gly Arg
252               230               235               240
254 gag gaa ggt atg gct gag gca tgg tac aat gcc att aca tcg gga tgg          884
255 Glu Glu Gly Met Ala Glu Ala Trp Tyr Asn Ala Ile Thr Ser Gly Trp
256           245               250               255
258 ggt cct gaa agt cct ctt tgg gat gat ttg gat agt tct cat cag ttt          932
259 Gly Pro Glu Ser Pro Leu Trp Asp Asp Leu Asp Ser Ser His Gln Phe
260       260               265               270
262 tca tca gaa agc tca tct tct tct cct ctc tct tgt cct atg agg cct          980
263 Ser Ser Glu Ser Ser Ser Ser Ser Pro Leu Ser Cys Pro Met Arg Pro
264 275               280               285               290
266 ttc ttt tga aaaagtttat aaacccacat tgtgttgtag gttatagttt              1029
267 Phe Phe  *
270 agggttatgc tcattggcat ttggatggag gcaatttttg tgatctccca ttccaccaca      1089
271 tatcagtcat tatatgtgtc taccttttct ctgtatttct atcattatca ttgtttttat      1149
272 tatgtgtctg tatgtgtttc cctattgcta catacataga tgtcctcttt gttcaaaaaa      1209
273 aaaaaaaaaa aaaaaaa                                                     1226
275 <210> SEQ ID NO: 4
276 <211> LENGTH: 292
277 <212> TYPE: PRT
278 <213> ORGANISM: Arabidopsis thaliana
280 <400> SEQUENCE: 4
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283 Val Asp His Ser Phe Gly Gly Glu Ala Ser Ser Thr Ser Pro Arg Ser
284               20               25               30
285 Met Lys Lys Met Lys Ser Pro Ser Arg Pro Lys Pro Tyr Phe Gln Ser
286           35               40               45
287 Ser Ser Ser Pro Tyr Ser Leu Glu Ala Phe Pro Phe Ser Leu Asp Pro
288       50               55               60
289 Thr Leu Gln Asn Gln Gln Gln Gln Leu Gly Ser Tyr Val Pro Val Leu
290 65               70               75               80
291 Glu Gln Arg Gln Asp Pro Thr Met Gln Gly Gln Lys Gln Met Ile Ser
292               85               90               95
293 Phe Ser Pro Gln Gln Gln Gln Gln Gln Gln Tyr Met Ala Gln Tyr
294               100               105               110
295 Trp Ser Asp Thr Leu Asn Leu Ser Pro Arg Gly Arg Met Met Met Met
296           115               120               125
297 Met Ser Gln Glu Ala Val Gln Pro Tyr Ile Ala Thr Lys Leu Tyr Arg
298       130               135               140
299 Gly Val Arg Gln Arg Gln Trp Gly Lys Trp Val Ala Glu Ile Arg Lys
300 145               150               155               160
301 Pro Arg Ser Arg Ala Arg Leu Trp Leu Gly Thr Phe Asp Thr Ala Glu
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/810,836B

DATE: 08/22/2002
TIME: 16:45:24

Input Set : A:\SEQLIST514442001200.TXT
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8/22/02